



1110> Hauptmann, Rudolph  
Hammler, Adolph  
Maurer-Foxy, Ingrid  
Stratowa, Christian

1310 90, 385-E

 $\cdot 14.0 \quad 0.525, 943$ 

61410-2000-06-15

0159 06, 383, 6 '6

$$0.1522 \pm 0.0017 = 0.2 = 0.1$$

150-03-151,2-7

1911 1015-11-17

15.000, 521,700

$$1510 = 1 \cdot 10^3 + 5 \cdot 10^2 + 0 \cdot 10^1 + 0 \cdot 10^0$$

<1500 07/511,4 -0

$$(1^0, 1^0) = (1, 1) + 0 = 0.4 = 0.0$$

(165) 87

© 2007 PatentIn Ver. 2.0

— 1 —

022. 1.03

222 DIA

2110 Homo sapiens

• 1991 (1) •

000000 CD8

000000 (1) .. (1369)

1000

(22) sau peptide

Q. 22. (1) .. (87)

1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 26

0.113 msec feature

$$\text{EQUATION (8)} \quad \bar{r} = (1, 0)$$

<123> Portion of TNF-BF pro protein cleaved by extracellular proteases following secretion.

4. 11.

&lt;\_.. miss feature

<222> · (606) .. (633)

<223> Portion of TNF- $\beta$  pro protein, cleaved by extracellular proteases following secretion.

400. 1

atg ggc ctc tcc acc gtg cct gac ctg ctg ctg cca ctg gtg ctc ctg	48
Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu	
1 5 10 15	
gag ctg ttg gtg gga ata tac tcc tca ggg gtt att gga ctg gtc cct	96
Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro	
20 25 30	
ccc ata ggg gac agg gag aag aca gat agt ggg tgt acc caa aga aaa	144
His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys	
35 40 45	
tat atc cac cct caa aat aat tgg att tgc tgt acc aag tgc cac aat	192
Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys	
50 55 60	
gga acc tac ttg tac aat gac tgt cca ggc cgg ggg cag gat acg gac	240
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp	
65 70 75 80	
tgc agg gag tgt gag agc ggc ttc ttc acc gct tca gaa aac cac ctc	288
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu	
85 90 95	
aga cac tgc ctc agc tgc tcc aca tgc cga aag gaa atg ggt cag gtg	336
Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val	
100 105 110	
gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg	384
Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg	
115 120 125	
aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag tgc ttc	432
Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe	
130 135 140	
aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc acc tgc cag gag	480
Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu	
145 150 155 160	
aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttc ata aga gaa	528
Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu	
165 170 175	
aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc aag	576
Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr	
180 185 190	
aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca	624
Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser	
195 200 205	
ggc aac aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt	672
Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu	
210 215 220	
tta tcc ctc ctc ttc att ggt tta atg tat cgc tac caa cgg tgg aag	720

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys	
225 230 235 240	
ttc aag ctg tac tcc att gtt tgt ggg aaa tgg aca cct gaa aaa gag	768
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Gln Lys Gln	
245 250 255	
ggg gag ctt gaa gga act act act aag ccc ctg ggc cca aac cca agc	816
Gly Glu Leu Gln Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser	
260 265 270	
ttc agt ccc act cca ggc ttc acc cac acc ctg ggc ttc agt ccc gtt	864
Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val	
275 280 285	
ccc agt tcc acc ttc acc tcc agt ttc acc tat acc ccc agt gac tgt	912
Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys	
290 295 300	
ccc aac ttt ggg ggt ccc cgc aga gag gtg gca cca ccc tat cag ggg	960
Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly	
305 310 315 320	
ggt gac ccc atc ctt ggg aca gcc ctg gcc tcc gag ccc atc ccc aac	1008
Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn	
325 330 335	
ccc ctt cag aag tgg gag gac agc gcc cac aag cca cag agc cta gag	1056
Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp	
340 345 350	
act gat gac ccc ggg aag ctg tac gcc gtg gtg gag aac gtg ccc cgg	1104
Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Gln Asn Val Pro Pro	
355 360 365	
ttg cgc tgg aag gaa ttc gtg cgg cgc cta ggg ctg agc gac cac gag	1152
Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu	
370 375 380	
atc gat cgg ctg gag ctg cag aac ggg cgc tgc ctg cgc gag ggc caa	1200
Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Gln Ala Gln	
385 390 395 400	
tac agc atg ctg ggg acc tgg aag cgg cgc acc cgg cgg tgc gag gcc	1248
Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala	
405 410 415	
aag ctg gag ctg ctg gga cgc gtg ctg cgc gac atg gac ctg ctg ggc	1296
Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly	
420 425 430	
tgt ctg gag gac atc gag gag gcc att tgc gcc ccc gcc gcc ctg cgg	1344
Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro	
435 440 445	
ccc ggc ccc agt ctt ctg aga tga	1368
Pro Ala Pro Ser Leu Leu Arg	

450

455

(210) 2  
 (211) 455  
 (212) IRT  
 (213) Homo sapiens

(400) 2

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
 1 5 10 15

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
 20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
 35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
 50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp  
 65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Gln Asn His Leu  
 85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Gln Met Gly Gln Val  
 100 105 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
 115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe  
 130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
 145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu  
 165 170 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr  
 180 185 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser  
 195 200 205

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu  
 210 215 220

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys  
 225 230 235 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu  
 245 250 255

Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser  
 260 265 270  
 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val  
 275 280 285  
 Pro Ser Ser Thr Phe Thr Ser Ser Thr Tyr Thr Pro Gly Asp Cys  
 290 295 300  
 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly  
 305 310 315 320  
 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn  
 325 330 335  
 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp  
 340 345 350  
 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro  
 355 360 365  
 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu  
 370 375 380  
 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln  
 385 390 395 400  
 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala  
 405 410 415  
 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly  
 420 425 430  
 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro  
 435 440 445  
 Pro Ala Pro Ser Leu Leu Arg  
 450 455

<210> 3  
 <211> 483  
 <212> DNA  
 <213> Homo sapiens

<210>  
 <211> CDS  
 <212> (1)..(483)

<410> 3  
 gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat tgg 48  
 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser  
 1 5 10 15  
 att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt 96  
 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys  
 20 25 30

cca acc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc 144  
 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser  
           35                          40                          45

ttc acc gct tca gaa aac sac ctc aga cac tgc ctc agc tgc tcc aaa 192  
 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys  
           50                          55                          60

tgc cga aag gaa atg ggt cag gtc gag atc tat tat tgc aca gtc gac 240  
 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp  
           65                          70                          75                          80

cag sac acc gtc tat ggc tgc aag aag aar cag tac cgg cat tat tgg 288  
 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp  
                           85                          90                          95

agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat gag 336  
 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly  
                           100                          105                          110

acc atc sac ctc tcc tgc cag gag aac cag aac acc gtc tgc acc tgc 384  
 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys  
                           115                          120                          125

cat cca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac 432  
 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn  
           130                          135                          140

tgt aag aac agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag 480  
 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu  
           145                          150                          155                          160

aat 483  
 Asn

<110> 4  
 <111> 161  
 <112> FRT  
 <113> Homo sapiens

<400> 4  
 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser  
   1                          5                          10                          15

Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys  
           20                          25                          30

Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser  
           35                          40                          45

Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys  
           50                          55                          60

Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp  
           65                          70                          75                          80

Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp  
85 90 95

Ser Gln Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly  
100 105 110

Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys  
115 120 125

His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn  
130 135 140

Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu  
145 150 155 160

Asn

<210>

<211> 7

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(87)

<300> 5

ttg agc ctc tcc acc gtg cct gac ctg ctg ctg cca ctg gtg ctc ctg 48  
Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
1 5 10 15

gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga 87  
Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly  
20 25

<310> 6

<311> 19

<312> PRT

<313> Homo sapiens

<400> 6

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
1 5 10 15

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly  
20 25

<410> 7

<411> 53

<412> DNA

<413> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(33)

<400> 7  
ctg gtc cct cgc cta ggg gac agg gag aag aga  
Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg  
1 5 10

33

<11> 8  
<11> 11  
<12> PRT  
<13> Homo sapiens

<400> 8  
Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg  
1 5 10

<10> 9  
<11> 30  
<12> DNA  
<13> Homo sapiens

<200>  
<210> CDS  
<222> (1)..(30)

<400> 9  
jtt aag ggc act gag gac tca ggc acc aca  
Val Lys Gly Thr Glu Asp Ser Gly Thr Thr  
1 5 10

30

<10> 10  
<11> 10  
<12> PRT  
<13> Homo sapiens

<400> 10  
Val Lys Gly Thr Glu Asp Ser Gly Thr Thr  
1 5 10

<10> 11  
<11> 1334  
<12> DNA  
<13> Artificial Sequence

<200>  
<210> CDS  
<222> (213)..(1325)

<230>  
<23> Description of Artificial Sequence: cDNA insert of  
lambdaTNF-BP15 and pTNF-BP15 vectors



<400> 11

gaattctctg gactgagget ccagttcttg cctttggggt tcaagatcac tgggaccagg 60  
 ccttgatctc tatgcagag cctcaccctt caactgtcac cccaggcac ttgggagctc 120  
 ctggacagac caggtccagg gaagcccccag cactggcgtt qccacactgc cctqagccca 180  
 aatggggagag ttagagggcca tagctgtctg gc atg ggc ctc tcc acc gtg cct 232  
 Met Gly Leu Ser Thr Val Pro  
 1 5  
 gac ctg ctg atg cca ctg gtg ctc ctg gag ctg ttg gtg gga ata tac 281  
 Asp Leu Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr  
 10 15 20  
 ccc tca ggg gtt att gga ctg gtc cct cac cta ggg gac agg gag aag 329  
 Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys  
 25 30 35  
 aga gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat 377  
 Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn  
 40 45 50 55  
 tgg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac 425  
 Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp  
 60 65 70  
 tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc 473  
 Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly  
 75 80 85  
 tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc 521  
 Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser  
 90 95 100  
 aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg 569  
 Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val  
 105 110 115  
 gac cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat 617  
 Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr  
 120 125 130 135  
 tgg agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat 665  
 Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn  
 140 145 150  
 ggg acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc 713  
 Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr  
 155 160 165  
 tgc cat gga ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt 761  
 Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser  
 170 175 180  
 aac tgt aag aaa agc ctg gag tgc acc aag ttg tgc cta ccc cag att 809

Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile  
 131 190 195

agg aat gtt aat ttc act gag gac tca ggt acc acc gta atg ttg ccc 887  
 Glu Asn Val Lys Gly Thr Gln Asp Ser Gly Thr Thr Val Leu Leu Pro  
 200 205 210 215

ctg gta att ttc ttt ggt ctt tgc ctt tta tcc ctc ctc ttc att ggt 905  
 Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly  
 220 225 230

tta atg tat cgc tac caa cgg tgg aag tcc aag ctc tac tcc att gtt 953  
 Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val  
 235 240 245

tgt ggg aaa tca aca cct gaa aaa gaa ggg gag ctt gaa gaa act act 1001  
 Cys Gly Lys Ser Thr Pro Gln Lys Gln Gly Gln Leu Glu Gly Thr Thr  
 250 255 260

act gag ccc atg gcc cca aac cca agc ttc agt ccc act cca ggc ttc 1049  
 Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe  
 265 270 275

acc ccc acc cag ggc ttc agt ccc gta ccc agt tcc acc ttc acc tcc 1097  
 Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser  
 280 285 290 295

agc tcc acc tat acc ccc ggt gac tgt ccc aac ttt gcg gct ccc cgc 1145  
 Ser Ser Thr Tyr Thr Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg  
 300 305 310

aga gag gtg gaa cca ccc tat cag ggg gct gac ccc atc ctt gcg aca 1193  
 Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr  
 315 320 325

gcc ctc gcc tcc gac ccc atc ccc aac ccc ctt cag aag tgg gag gac 1241  
 Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp  
 330 335 340

agc gcc cac aag cca cag agc cta gac act gat gac ccc gcg acg ctg 1289  
 Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu  
 345 350 355

tac gcc gtg gtg gag aac gtg ccc ccg ttg cgc tgg aaggaattc 1334  
 Tyr Ala Val Val Gln Asn Val Pro Pro Leu Arg Trp  
 360 365 370

<210> 12

<211> 371

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: cDNA insert of  
 lambdaTNF-BP15 and pTNF-BP15 vectors

<400> 12

Met Gly Leu Ser Thr Val Pro A.p Leu Leu Leu Pro Leu Val Leu Leu  
1 5 10 15

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp  
65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
100 105 110

Glu Ile Ser Ser Cys Thr Val A.p Arg Asp Thr Val Cys Gly Cys Arg  
115 120 125

Lys Asn Gln Tyr Arg His Tyr Tip Ser Glu Asn Leu Phe Gln Cys Phe  
130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu  
165 170 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr  
180 185 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser  
195 200 205

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu  
210 215 220

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys  
225 230 235 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu  
245 250 255

Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser  
260 265 270

Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val  
275 280 285

Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys  
290 295 300

Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly  
305 310 315 320

Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Ile Ile Phe Asn  
325 330 335

Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp  
340 345 350

Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro  
355 360 365

Leu Arg Trp  
370

4210: 13  
4211: 6414  
4212: DNA  
4213: Artificial Sequence

4220:  
4221: Description of Artificial Sequence: pADCMV1 vector

4230:  
4231: unsure  
4232: (344)  
4233: "n" can be a, g, c, or t

4240:  
4241: unsure  
4242: (4157)  
4243: "n" can be a, g, c, or t

4250:  
4251: unsure  
4252: (5135)  
4253: "n" can be a, g, c, or t

4260:  
4261: unsure  
4262: (6255)  
4263: "n" can be a, g, c, or t

4400: 13  
tggacattga ttattgacta gttattaata gtaatcaatt acggggtgat tagttcatag 60  
cccatatatg gagttccggg ttacataact tacggtaaat ggcccgcctc gctgaccgcc 120  
cgaagacccc cggccattga cgtcaataat gacgtatggt cccatagtaa cggcaatagg 180  
gactttccat tgaagtcgat ggggtggagta tttacggtaa actgcccaact tggcagtaga 240  
tcaaagtgtat catatgccaa gtaagccccc tattgacgtc aatgacggta aatggccggc 300  
ctgggattat gccacgtaca tgacattatg ggactttcct actnggcagt acattctagt 360

attagtcate gctattacca tgggtatgag gttttggag tacctcaatg ggggtggata 420  
 aggttttgac tcaaggggat ttccaagtct ccacccatt gacgtcaatg ggaatttgtt 480  
 ttggcaccaa aatcaacggg actttccaaa atgttgtaac aactccccc ctttgacgca 540  
 aatggggggg aggggtgtac ggtgggaggt ctatataagg agagctctct ggttaactag 600  
 agaacccact gcttaactgg cttatcgaaa ttaatacgac tcactatagg gacacccaaq 660  
 cttctgcagg tggacataga tggatccggt aactcgagcg cgaattctct apaggatctt 720  
 tgtgaaggaa ccttaactct gtggttgac ataattggac aaactacata cagagattta 780  
 aagctctaug gtaaatataa aatttttaag tgtataatgt gttaaactac tgattetaat 840  
 tgttttgta ttttagatto caacctatgg aactgatgaa tgggagcagt ggtggaatgc 900  
 atttaatgag gaaaacctgt tttgctcaga agaaatgcca tctagtgatg atgaggetac 960  
 tctgactct caacattcta ctctccaaa aaagaagaga aaggtagag agcccaagga 1020  
 ctttccctca gaattgctaa gttttttgag tcatgtgtg tttagtata gaactcttgc 1080  
 ttgctttgct attacacca caaaggaaaa agctgcactg ctatacaga aaattatgga 1140  
 aaaatatttg atgtatagtg ccttgactag agatcataat cagccatacc acattttag 1200  
 aggttttaet tgctttaaaa aactccccc aactccccc gaacctgaaa cataaaatga 1260  
 atgcaattgt tgtgttaac ttgtttattg cagcttataa tggttacaaa taaagcaata 1320  
 gcatcacaaa ttccacaaat aaagcatttt ttccactgca tctagttgt ggtttgtcca 1380  
 aactcacaai tgtatcttat catgtctgga tcaattctga gaaactagcc ttaaagacag 1440  
 acagctttgt tctagtcage caggcaagca tatgtaaata aagttctca gggaaatgag 1500  
 gttaaaagat gtatcttga cctgcacag cttggcattc acgtaaacag aagattccgc 1560  
 ctcaagttcc ggttaacaa aggaggcaac gagatctcaa atctattact tctaactggg 1620  
 taattaaaaa ctttaacta aaacacggac caacggatgt caccacttt tcttccccc 1680  
 gctcccccct tctagtaet cccaccatt aggtctgcta ctccactcc atttccgggc 1740  
 ggcacacca cgtgcctct cccaccgac gctaaccocg cccctgcgcg tctaaccccg 1800  
 cccaccact ggcocccccc cgttgaggac agaagaaaa cgggagagcc gacgcaagg 1860  
 cggaggggtg gacgtgggg ggcgtgagga gtgtctctt acctctctg ctggctcggg 1920  
 gggggaocgg gtggatctca ggttccgga gaactggaag aacgggtca gaacgcttg 1980  
 tctccgggg gtttggggg cggagaagt ggcgtagac gggacttg tgagagcat 2040

agcaggatgc agaagagcaa gccgcgcggg agcgcgcggc tgaactacc cgcgcctgga 2100  
 cgcgcacgc cggactgggc ggggcgcggc tggcggagc ggaactcga ctcgtcggg 2160  
 agcgcgcgcgc agcgcgcgcgc gactgcgcgc tgcgcgcgcgc ctcgcgcgcgc ggcgcgcgcgc 2220  
 cgcgcgcgcgc agcgcgcgcgc tgcgcgcgcgc atgcgcgcgc cgcgcgcgcgc cgcgcgcgcgc 2280  
 ggcgcgcgcgc atgcgcgcgc cgcgcgcgcgc ggcgcgcgcgc ctcgcgcgcgc ggcgcgcgcgc 2340  
 tgcgcgcgcgc ggcgcgcgcgc aacgcgcgcgc ggcgcgcgcgc tgcgcgcgcgc cgcgcgcgcgc 2400  
 agcgcgcgcgc ggcgcgcgcgc tgcgcgcgcgc cgcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc 2460  
 tgcgcgcgcgc ggcgcgcgcgc tgcgcgcgcgc cgcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc 2520  
 tgcgcgcgcgc cgcgcgcgcgc cgcgcgcgcgc tgcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc 2580  
 ggcgcgcgcgc tgcgcgcgcgc ggcgcgcgcgc aacgcgcgcgc ctcgcgcgcgc tgcgcgcgcgc 2640  
 ggcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc cgcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc 2700  
 ggcgcgcgcgc aacgcgcgcgc aacgcgcgcgc cgcgcgcgcgc tgcgcgcgcgc ggcgcgcgcgc 2760  
 cgcgcgcgcgc atgcgcgcgc aacgcgcgcgc cgcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc 2820  
 ggcgcgcgcgc aacgcgcgcgc tgcgcgcgcgc ggcgcgcgcgc cgcgcgcgcgc ggcgcgcgcgc 2880  
 tgcgcgcgcgc ggcgcgcgcgc atgcgcgcgc aacgcgcgcgc cgcgcgcgcgc ggcgcgcgcgc 2940  
 ggcgcgcgcgc ggcgcgcgcgc tgcgcgcgcgc ggcgcgcgcgc aacgcgcgcgc ggcgcgcgcgc 3000  
 aggcgcgcgc agcgcgcgcgc tgcgcgcgcgc cgcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc 3060  
 cgcgcgcgcgc ggcgcgcgcgc aacgcgcgcgc cgcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc 3120  
 aggcgcgcgc ggcgcgcgcgc tgcgcgcgcgc atgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc 3180  
 ggcgcgcgcgc tgcgcgcgcgc cgcgcgcgcgc tgcgcgcgcgc cgcgcgcgcgc ggcgcgcgcgc 3240  
 tgcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc atgcgcgcgc ggcgcgcgcgc 3300  
 tgcgcgcgcgc tgcgcgcgcgc cgcgcgcgcgc cgcgcgcgcgc atgcgcgcgc ggcgcgcgcgc 3360  
 tgcgcgcgcgc cgcgcgcgcgc ggcgcgcgcgc atgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc 3420  
 ggcgcgcgcgc tgcgcgcgcgc cgcgcgcgcgc cgcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc 3480  
 ggcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc 3540  
 ggcgcgcgcgc agcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc 3600  
 ggcgcgcgcgc aacgcgcgcgc tgcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc 3660  
 ggcgcgcgcgc tgcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc aacgcgcgcgc ggcgcgcgcgc 3720  
 ggcgcgcgcgc tgcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc ggcgcgcgcgc 3780

ttaacttctc cgtttctcat cttcagtgag attccaaggg ataactacaat tctgtggaat 3840  
 gtgtgtcagt taggggtgtg aaagtcccca ggctcccca caggtcagaat tatgcacacg 3900  
 atgcattctca attagtccgc aaccaggtgt ggaaagtccc caggtccccc agcagggcaga 3960  
 agtatgcaca gcatgcattt caattagtcg gcaacatag tcccgccctt aactccgcgc 4020  
 atccagcccc taactcgcgc cagttccgcg cattctcgcg ccaatggctg actaatTTTT 4080  
 tttatttatg cagagggcga ggccctcttg agctattcca gaaqtagtga ggagggtttt 4140  
 ttggaggcct aggtttntgc aaaaaagcta attcagcttg aatggcgatg gggacgcgcg 4200  
 ctgtagcggc gcattaagcg cggcggtgt ggtggttaag cgcagcgtga ccgtacact 4260  
 tgcagcgccg ctacgcgcgc ctccttctgc tttattcctt cctttctcgc ccaagttcgc 4320  
 cggctttccc cgtcaagctc taaatcgggg gctcccttta gggttcccat ttatgtttt 4380  
 accgtacctc gacccccaaa acttgattag ggtgatgggt cactgaqtgg gccatgcgcg 4440  
 tgatagaagg ttttcgcgc ttgacgttg gagtccaggt cctttaatag tggactcttg 4500  
 ttccaaaact gaacaacact caaccctatc tgggtctatt ctttgattt ataagggatt 4560  
 ttgcgcattt cggcctattg gttaaaaaat gagctgattt aacaaaaatt taacgcgaat 4620  
 ttttaaaaaa tattaacgtt tacaattcca ggtggcactt ttgggggaaa tgtgcgggga 4680  
 accctattt gttattttt ctaaatacat tcaaatatgt atccgctcat gagacaataa 4740  
 ccttgataaa tgcctcaata atattgaaaa aggaagagta tgagtattca acatttcctg 4800  
 gtgcgcctta ttcccttttt tggggcattt tgccttcttg cctttgctca ccagaaaaag 4860  
 ctggtgaaaag taaaagatgc tgaagatcag ttgggtgcac gagtgggcta catcgaaact 4920  
 gatcccaaca ggggtaagat ccttgagagt ttgcgcgcg aagaacgttt tccaatgatg 4980  
 agcaatttta aagttctgct atgtggcgcg gtattatccc gtattgacgc cgggcaagag 5040  
 caactcggtc gcgcataca ctattctcag aatgacttgg ttgagtactc accagtcaca 5100  
 gaaaagcact ttaaggatgg catgacagta agagnattat gcagtgtgc cacaaccatg 5160  
 agtgataaca ctggggccaa cttactcttg acaacgatcg gaggacgaa ggagctaacg 5220  
 gcttttttgc acaacatggg ggatcatgta actcgccttg atcgttggga accggagctg 5280  
 aatgaagcca taccaaaaga cgagcgtgac accacgatgc ctgtagcaat ggcacaaacg 5340  
 ttgcgcaaac tattaactgg cgaactactt actctagctt ccgggcaaca attaatagac 5400  
 tggatggagg cggataaagt tgcaggacca cttctgcgtt cggccttcc ggcgtggtgg 5460

tttattgctg ataaatctgg agcgggtgag cgtgggtctc gggglatcat tgragcactg 5520  
 gggecagatg gtaagccctc cegtatcgta gttatctaca cgaaggggag ttaggcaact 5580  
 atgatatcaat aaatataca gatctctag ataggtgact caatgattaa gatttggtaa 5640  
 ctgtcagacc aagtttactc atataactt tagattgatt taaaacttca tttttaattt 5700  
 aaaaggatct aggttaagat cctttttgat aatctcatga ccaaaatcc tttaagtgag 5760  
 ttttggttcc actgagcgta agaccccgta gaaaagatca aaggatcttc ttgagatcct 5820  
 tttttcttgc gggtaactct cgtgttgcaa acaaaaaaac caccgtacc agtggtaggt 5880  
 tgttgccggg atcaagagct accaactctt tttccgaagg taactggctt cagcagagcg 5940  
 caataacca atactgtctt tctagtgtag ccttagttag gccaccactt caagaactct 6000  
 gtagcaccgc ctatatact cgtcttgata atctgttac cagtggctgc tgcgaatggt 6060  
 gataagtcgt gtcttaccgg gtggactca agacgatagt taccggataa ggcgcagcgg 6120  
 tctggctgaa cgggggggtc gtgcacacag ccagcttgg agcgaacgac ctacaccgaa 6180  
 ctgagatacc taacagctga gcattgagaa agcggcaccg ttcccgaagg gagaaggcg 6240  
 gaaadgtatc cggtnagcgg cagggtcgga acaggagagc gcacgaggga gcttccaggg 6300  
 ggaaacgcct ggtatcttta tagtctgtc ggggttcgcc acctctgact tgagcgtcga 6360  
 ttttgggat gctcgtcagg gggggcggag ctagggaaa acgcccagcaa cgc 6414

<110> 14  
 <111> 2173  
 <112> DNA  
 <113> Artificial Sequence

<110>  
 <111> CDS  
 <112> (245)..(1630)

<120>  
 <121> Description of Artificial Sequence: raTNF-R8

<400> 14  
 gaattccttt tctccagatt ttctgaactc tggctcatga tgggcttac tggatacag 60  
 aatctggag gacgtacc tgatttccat ctacctctga ctttgacct ttctaaccgt 120  
 gggtcaccgc tgcacacacc cgggcacact ggtccgatcg tcttacttca ttcaccagcg 180  
 ttgccaattg ctgcctctgc ccagcccca atgggggagt gagagagcc actgcgcgcc 240  
 ggac atg ggt ctc ccc atc gtg cct ggc ctg ctg ctg tca ctg gtg ctc 280  
 Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu  
 1 5 10 15



atg get atg atg atg ggg ata cac cca tca ggg gtc acc gga atg gtt	337
Leu Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu Val	
20 25 30	
cct tct ctt ggt gac agg gag aag agg gat aat ttg tgt ccc cag gga	385
Pro Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly	
35 40 45	
aag tat gcc cat cca aag aat aat tcc atc tcc tgc acc aag tgc cac	433
Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His	
50 55 60	
aaa gga acc tcc ttg gtg agt gac tgt cca acc cca ggg cag gaa acc	481
Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr	
65 70 75	
gtc tgc gag ctc tct cat aac ggc acc ttt acc gct tcc cag aac cac	529
Val Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His	
80 85 90 95	
gtc aga cag tgt ctc aat tgc aag aca tgt cgg aaa gaa atg ttc cag	577
Val Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln	
100 105 110	
gtg gag att cct cct tcc aaa gct gac atg gac acc gtg tgt gcc tgc	625
Val Glu Ile Ser Pro Cys Lys Ala Asp Met Asp Thr Val Cys Gly Cys	
115 120 125	
aag aag aac caa ttc cag cgc tcc atg agt gag acg cat ttc cag tgt	673
Lys Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His Phe Gln Cys	
130 135 140	
gtg gac tgc agc ccc tcc ttc aat ggc acc gtg aca atc ccc tgt aag	721
Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys	
145 150 155	
gag aaa cag aac acc gtg tgt aac tgc cac gca gga ttc ttt cta agc	769
Glu Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser	
160 165 170 175	
gga aat gag tgc acc cct tgc agc cac tgc aag aaa aat cag gaa tgt	817
Gly Asn Glu Cys Thr Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys	
180 185 190	
atg aag atg tgc cta cct cca gtt gca aat gtc aca aac ccc cag gac	865
Met Lys Leu Cys Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp	
195 200 205	
tca ggt act gcc gtg atg ttg cct atg gtt atc ttc cta ggt att tgc	913
Ser Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu Gly Leu Cys	
210 215 220	
att tta ttc ttt atc tgc atc aat cta atg tgc cga tat ccc cag tgg	961
Leu Leu Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp	
225 230 235	

agg ccc agg gtc tac tcc atc att tgt agg gat tca gct cct gtc aaa 1009  
 Arg Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys  
 240 245 250 255  
 acc gta aac att caa gga att att act aag cca cta act caa ggc tct 1057  
 Glu Val Glu Gly Glu Gly Ile Val Thr Lys Pro Leu Thr Ile Ala Ser  
 260 265 270  
 atc cca gac ttc aac ccc aac ccc ggc ttc aac ccc act cta ggc ttc 1105  
 Ile Pro Ala Phe Ser Pro Asn Pro Gly Phe Asn Pro Thr Leu Gly Phe  
 275 280 285  
 age aac aac cca ccc ttc agt cat cct gta tcc agt aac ccc atc age 1153  
 Ser Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr Pro Ile Ser  
 290 295 300  
 ccc gtc ttc ggt cct agt aac tgg cac aac ttc gtc cca cct gta aga 1201  
 Pro Val Phe Gly Pro Ser Asn Trp His Asn Phe Val Pro Pro Val Arg  
 305 310 315  
 gag gtg gtc cca aac cag ggt gct gac cct ctc ctc tac gga tcc ctc 1249  
 Glu Val Val Pro Thr Glu Gly Ala Asp Pro Leu Leu Tyr Gly Ser Leu  
 320 325 330 335  
 aac cct gtg cca atc ccc gcc cct gtt cgg aaa tgg gaa gac gtc gtc 1297  
 Asn Pro Val Pro Ile Pro Ala Pro Val Arg Lys Trp Glu Asp Val Val  
 340 345 350  
 gcg gcc cag cca caa cgg ctt gac act gca gac cct gcg atg ctg tat 1345  
 Ala Ala Gln Pro Gln Arg Leu Asp Thr Ala Asp Pro Ala Met Leu Tyr  
 355 360 365  
 get gtg gtg gat gcc gtg cct cgg aca cgg tgg aag gag ttc atg cgg 1393  
 Ala Val Val Asp Gly Val Pro Pro Thr Arg Trp Lys Glu Phe Met Arg  
 370 375 380  
 ctc ctg ggg ctg agc gag cac gag atc gag cgg ttg gag ctg cag aac 1441  
 Leu Leu Gly Leu Ser Glu His Glu Ile Glu Arg Leu Glu Leu Gln Asn  
 385 390 395  
 ggg cgt tgc ctc cgc gag got cat tac agc atg ctg gaa gcc tgg cgg 1489  
 Gly Arg Cys Leu Arg Glu Ala His Tyr Ser Met Leu Glu Ala Trp Arg  
 400 405 410 415  
 cgc cgc aca ccc cca cac gag gcc aac ctg gac gta gtg gcc cgg gtg 1537  
 Arg Arg Thr Pro Arg His Glu Ala Thr Leu Asp Val Val Gly Arg Val  
 420 425 430  
 ctt tgc gac atg aac ctg cgt ggc tgc ctg gag aac atc cgc gag act 1585  
 Leu Cys Asp Met Asn Leu Arg Gly Cys Leu Glu Asn Ile Arg Glu Thr  
 435 440 445  
 cta gaa age cct gcc cac tgc tcc aac aac cac ctc cgc cga taa 1630  
 Leu Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro Arg  
 450 455 460

ggccacaccc ccacctcagg aacgggaactc gaaggaccat cctgctagat gccctgcttc 1690

cctgtgaacc tectcttttg tectctaggg ggcaggctcg atctggcagg ctgatcttg 1750  
 cagcacttc cttgggtgta ccgacttggg gtacatagct ttcccagct gccagggaac 1810  
 gcctgtgaca gccacttgtg catggcaggg aagtgtgaca tctgctaca gacagctgag 1870  
 ggtgccaaaa gccaggagag gtgatttggg agaaaaagca caatctatct gatacccact 1930  
 tgggatgcaa ggaacccaaag aaagcttctc agggctctct cagttgatit ctgggccttt 1990  
 ttccagtag ataaaaacgt ctttgtattg atttatcac actaatggat gaacggttga 2050  
 actccctaag gtaggggcaa gcacagaaca gtggggtctc cagctggagc ccccgactct 2110  
 tgtaaataca ctaaaaatct aaaagtgaac aaaaaaaaaa aaaaaaaaaa aaagaaggaa 2170  
 ttc 2173

<210> 15  
 <211> 461  
 <212> PRT  
 <213> Artificial Sequence

<210>  
 <213> Description of Artificial Sequence: raTNF-R3

<400> 15  
 Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu Leu  
 1 5 10 15  
 Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu Val Pro  
 20 25 30  
 Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly Lys  
 35 40 45  
 Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
 50 55 60  
 Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val  
 65 70 75 80  
 Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val  
 85 90 95  
 Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln Val  
 100 105 110  
 Gln Ile Ser Pro Cys Lys Ala Asp Met Asp Thr Val Cys Gly Cys Lys  
 115 120 125  
 Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His Phe Gln Cys Val  
 130 135 140  
 Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys Glu

145		150		155		160
Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly						
	165			170		175
Asn Glu Cys Thr Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys Met						
	180			185		190
Lys Leu Cys Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp Ser						
	195			200		205
Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu Gly Leu Cys Leu						
	210			215		220
Leu Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg						
	225			230		235
Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys Glu						
	245			250		255
Val Glu Gly Glu Gly Ile Val Thr Lys Pro Leu Thr Pro Ala Ser Ile						
	260			265		270
Pro Ala Phe Ser Pro Asn Pro Gly Phe Asn Pro Thr Leu Gly Phe Ser						
	275			280		285
Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr Pro Ile Ser Pro						
	290			295		300
Val Phe Gly Pro Ser Asn Trp His Asn Phe Val Pro Pro Val Arg Glu						
	305			310		315
Val Val Pro Thr Gln Gly Ala Asp Pro Leu Leu Tyr Gly Ser Leu Asn						
	325			330		335
Pro Val Pro Ile Pro Ala Pro Val Arg Lys Trp Glu Asp Val Val Ala						
	340			345		350
Ala Gln Pro Gln Arg Leu Asp Thr Ala Asp Pro Ala Met Leu Tyr Ala						
	355			360		365
Val Val Asp Gly Val Pro Pro Thr Arg Trp Lys Glu Phe Met Arg Leu						
	370			375		380
Leu Gly Leu Ser Glu His Glu Ile Glu Arg Leu Glu Leu Gln Asn Gly						
	385			390		395
Arg Cys Leu Arg Glu Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg						
	405			410		415
Arg Thr Pro Arg His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu						
	420			425		430
Cys Asp Met Asn Leu Arg Gly Cys Leu Glu Asn Ile Arg Glu Thr Leu						
	435			440		445
Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro Arg						

450

455

460

<210> 16  
 <211> 1141  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (213)..(1180)

<220>  
 <223> Description of Artificial Sequence: human TNF-R in  
 ITNF-R2

<400> 16  
 gattttcttg gactgagcct ccagttcttg ccttgggggt tcaagatcac tgggaccagg 60  
 cgttgatctc tatgcccgag tctcaacct caactgtcac cccaaggcac ttgggacgtc 120  
 ctggacacac cgagtcctcg gaagccccag cactgctcgt gccacactgc cctgagccca 180  
 katgggggag tgagaggcca tagctgtctg gc atg ggc ctc tca acc gtg cct 232  
 Met Gly Leu Ser Thr Val Pro  
 1 5  
 gac ctg ctg ctg cca ctg gtg ctc ctg gag ctg ttg gtg gga ata tac 281  
 Asp Leu Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr  
 10 15 20  
 ccc tca ggg gtt att gga ctg gtc cct cac cta ggg gac agg gag aag 329  
 Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys  
 25 30 35  
 aga gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat 377  
 Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn  
 40 45 50 55  
 tgg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac 425  
 Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp  
 60 65 70  
 tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc 473  
 Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly  
 75 80 85  
 tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc 521  
 Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser  
 90 95 100  
 aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg 569  
 Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val  
 105 110 115  
 gac cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat 617  
 Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr

120	125	130	135	
tgg agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat				605
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn	140	145	150	
ggg aac gtg cac ctc tcc tgc cag gag aac cac aac aac gtg tgc aac				715
Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr	155	160	165	
tgc cat gca agt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt				761
Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser	170	175	180	
aac tat aag aaa agc ctc gag tgc acg aag ttg tgc cta ccc aag att				809
Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile	185	190	195	
gag aat gtt aag agc act gag gac tca ggt aac aac gtg ctc ttg ccc				855
Gln Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro	200	205	210	215
ctg gtc att ttc ttt ggt ctt tgc ctt tta tcc ctc ctc ttc att ggt				905
Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly	220	225	230	
tta atg tat cgc tac caa cgg tgg aag tcc aag ctc tac tcc att gtt				955
Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val	235	240	245	
tgt ggg aaa tgc aca cct gaa aaa gag ggg gag ctt gaa gga act act				1001
Cys Gly Lys Ser Thr Pro Glu Lys Gln Gly Glu Leu Glu Gly Thr Thr	250	255	260	
act aag ccc ctg gcc cca aac cca agc ttc agt ccc act cca gcc ttc				1049
Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe	265	270	275	
acc ccc acc ctg ggc ttc agt ccc gtg ccc agt tcc acc ttc acc tcc				1097
Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser	280	285	290	295
agc tcc acc tat acc ccc ggt gac tgt ccc aac ttt gcg gct ccc cgc				1145
Ser Ser Thr Tyr Thr Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg	300	305	310	
aga gag gtg gca cca ccc tat cag ggg gct gac ccc atc ctt gcg aca				1193
Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr	315	320	325	
gcc ctc gcc tcc gag ccc atc ccc aac ccc ctt cag aag tgg gag gac				1241
Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp	330	335	340	
agc gcc cac aag cca cag agc cta gac act gat gac ccc gcg acg ctc				1289
Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu	345	350	355	

tac gcc gtg gtg gag aac gtg ccc ccc ttg cgc tgg aag gaa ttc gtg 1337  
Tyr Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val  
350 365 370 375

cgg cgc cta ggg ctg agc gar ccc gag atc gat cgg ctg gag ctg cag 1385  
Arg Arg Leu Gly Leu Ser Asp His Glu Ile Asp Arg Leu Glu Leu Glu  
380 385 390

aac ggg cgc tgc ctg cgc gag gag cca tac agc atg ctg gag acc tgg 1433  
Asn Gly Arg Cys Leu Arg Glu Ala Glu Tyr Ser Met Leu Ala Thr Trp  
395 400 405

cgg cgg cgc acc ccc cgg cgc gag gcc acc ctg gag ctg ctg gaa cgc 1481  
Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu Leu Gly Arg  
410 415 420

gtg ctg cgc gac atg gag ctg ctg ggc tgc ctg gag gar atc gag gag 1529  
Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu  
425 430 435

ggc att tgc ggc ccc gcc gcc ctc ccc ccc ggc ccc agt att ctg aga 1577  
Ala Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg  
440 445 450 455

tga ggctggcgccc ctgggggcag ctctaaggac cgtctgcga gatcgcttc 1630

caacccccact tttttctgga aaggaggggt cctgcagggg caagcaggag ctacgagccg 1690

cctacttggg gctaaccct ccatgtacat agctttctc agctgcctgc ggcgcgcga 1750

cagtcagcgc tctgcgcgcg gagagaggtg cgcctgtggc tcaagagcct gagtgggtgg 1810

ttgcgagga tgagggaagc tatgcctcat gcccgcttg ggtgtctca ccagcaaggc 1870

tgtcggggg cccctggttc gtccctgagc ctttttcaca gtgcataagc agttttttt 1930

gtttttgttt tgttttgttt tgtttttaa tcaatcatgt tacactaata gaaacttggc 1990

actcctgtgc cctctgcctg gacaagcaca tagcaagctg aactgtccta aggcaggggc 2050

gagcaaggaa caatgggggc ttcagctgga gctgtggact ttgtacata cactaaaatt 2110

ctgaagttaa aaaaaaaaaa aaaaggaatt c 2141

<210> 17

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: human TNF-R in  
1TNF-R2

<400> 17

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
 1 5 10 15  
 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
 20 25 30  
 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
 35 40 45  
 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
 50 55 60  
 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp  
 65 70 75 80  
 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
 85 90 95  
 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
 100 105 110  
 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
 115 120 125  
 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe  
 130 135 140  
 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
 145 150 155 160  
 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu  
 165 170 175  
 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr  
 180 185 190  
 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser  
 195 200 205  
 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu  
 210 215 220  
 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys  
 225 230 235 240  
 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu  
 245 250 255  
 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser  
 260 265 270  
 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val  
 275 280 285  
 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys  
 290 295 300



Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly  
305 310 315 320

Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn  
325 330 335 340

Pro Leu Glu Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp  
340 345 350

Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro  
355 360 365

Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu  
370 375 380

Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln  
385 390 395 400

Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala  
405 410 415

Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly  
420 425 430

Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro  
435 440 445

Pro Ala Pro Ser Leu Leu Arg  
450 455

<210> 18

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<221> Description of Artificial Sequence: N-terminal  
amino acid sequence of protein purified from urine  
(main sequence)

<222>

<223> UNSURE

<224> (4)

<225> Identity of "Xaa" could not be determined.

<400> 13

Asp Ser Val Xaa Pro Gln Gly Lys Tyr Ile His Pro Gln  
1 5 10

<210> 19

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: N-terminal  
amino acid sequence of protein purified from urine  
(subsidiary sequence)

<240>

<241> UNSURE

<242> (7)

<243> Identity of "Xaa" could not be determined.

<400> 19

Leu Val Pro His Leu Gly Xaa Arg Glu

<210> 16

<211> 151

<212> DNA

<213> Homo sapiens

<400> 16

cacdegaaaa tattenccct caaataattc gatttgcgtg accaagtgcg acaaaggaaa 60

ctactctaac aatgaactct caggeccggg gcaggatacg gactgcaggg agtgtgagag 120

cgactcttc acagctcag aaaacaacaa g 151

<210> 21

<211> 5

<212> PRT

<213> Artificial Sequence

<240>

<243> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 21

Asp Ser Val Cys Pro Gln Gly Lys

1

5

<210> 22

<211> 7

<212> PRT

<213> Artificial Sequence

<240>

<243> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<240>

<241> UNSURE

<242> (1)..(2)

<243> Identity of "Xaa" could not be determined.

<400> 22

Xaa Xaa Leu Ser Cys Ser Lys

<210> 23  
<211> 7  
<212> PPT  
<213> Artificial Sequence

<220>  
<221> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 23  
A p Thr Val Cys Gly Cys Arg  
1 5

<110> 24  
<111> 11  
<112> PPT  
<113> Artificial Sequence

<220>  
<221> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 24  
Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys  
1 5 10

<110> 25  
<111> 12  
<112> PPT  
<113> Artificial Sequence

<220>  
<221> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 25  
Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys  
1 5 10

<110> 26  
<111> 13  
<112> PPT  
<113> Artificial Sequence

<220>  
<221> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<120>  
<121> UNSURE  
<222> (6)

<223> Identity of "Xaa" could not be determined.

<220>

<221> UNSURE

<212> PRT

<223> Identity of "Xaa" could not be determined.

<400> 26

Tyr Ile His Pro Gln Xaa Asn Ser Ile Xaa Xaa Xaa Lys

1

5

10

<210> 27

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 27

Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys

1

5

10

<210> 28

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 28

Leu Val Pro His Leu Gly Asp Arg

1

5

<210> 29

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 29

Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg

1

5

10

15

<210> 30

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 30

His Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln  
1 10

<210> 31

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<220>

<221> UNSURE

<222> (9)..(11)

<223> Identity of "Xaa" could not be determined.

<400> 31

Glu Met Gly Gln Val Glu Ile Ser Xaa Xaa Xaa Val Asp  
1 5 10

<210> 32

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 32

Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp  
1 5 10 15

Thr Val Cys Gly  
20

<210> 33

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<220>

<221> UNSURE

<222> (6)

<223> Identity of "Xaa" could not be determined.

<224>

<225> UNSURE

<226> (18)

<227> Identity of "Xaa" could not be determined.

<228>

Tyr Ile His Pro Gln Xaa Asn Ser Ile Cys Cys Thr Lys Cys His Lys

1

5

10

15

Gly Xaa Tyr

<229> 34

<230> 18

<231> PFT

<232> Artificial Sequence

<233>

<234> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<235>

<236> UNSURE

<237> (16)..(17)

<238> Identity of "Xaa" could not be determined.

<239> 34

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Xaa

1

5

10

15

Xaa Arg

<240> 35

<241> 8

<242> PFT

<243> Artificial Sequence

<244>

<245> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<246> 35

Leu Cys Leu Pro Gln Ile Glu Asn

1

5

<247> 36

<248> 14

<249> PFT

<250> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<220>

<221> UNSURE

<222> (7)

<223> Identity of "Xaa" could not be determined.

<400> 36

Gln Asn Thr Val Cys Thr Xaa His Ala Gly Phe Phe Leu Arg  
1 5 10

<210> 37

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 37

Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn  
1 5 10

<210> 38

<211> 15

<212> PRT

<213> Homo sapiens

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 38

Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln  
1 5 10

<210> 39

<211> 7

<212> PRT

<213> Homo sapiens

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 39

Gln Gly Lys Tyr Ile His Pro  
1 5

<210> 40  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 40  
caaggtaaat atatccatcc 10

<210> 41  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 41  
caaggtaaat acatccatcc 20

<210> 42  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 42  
caaggtaaat atatacatcc 20

<210> 43  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 43  
caaggtaaat atattcatcc 20

<210> 44  
<211> 20  
<212> DNA  
<213> Artificial Sequence



<220>

<221> Description of Artificial Sequence: Hybridization  
probe

<400> 44

caacccaaagt acatccaccc

20

<210> 45

<211> 20

<212> DNA

<213> Artificial Sequence

<210>

<211> Description of Artificial Sequence: Hybridization  
probe

<400> 45

caacccaaagt atataaatcc

20

<210> 46

<211> 20

<212> DNA

<213> Artificial Sequence

<210>

<211> Description of Artificial Sequence: Hybridization  
probe

<400> 46

caacccaaagt atattcattc

20

<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

<210>

<211> Description of Artificial Sequence: Hybridization  
probe

<400> 47

caacccaaagt acatccaccc

20

<210> 48

<211> 20

<212> DNA

<213> Artificial Sequence

<210>

<211> Description of Artificial Sequence: Hybridization  
probe

<400> 48

caagggaat atatacatcc

20

<210> 49 \

<211> 20

<212> DNA

<213> Artificial Sequence

<221>

<223> Description of Artificial Sequence: Hybridization  
probe

<401> 49

caagggaat atatacatcc

20

<210> 50

<211> 20

<212> DNA

<213> Artificial Sequence

<221>

<223> Description of Artificial Sequence: Hybridization  
probe

<401> 50

caagggaagt acatccacccc

20

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization  
probe

<401> 51

caagggaat atatacatcc

20

<210> 52

<211> 14

<212> PRT

<213> Artificial Sequence

<221>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<401> 52

Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys

1

5

10

<210> 53

<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 53  
Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Cys Asn Asn Lys  
1 10

<210> 14  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 14  
Phe Thr Ala Ser Glu Asn Asn Lys  
1 5

<210> 55  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 55  
Phe Thr Ala Ser Cys Asn Asn Lys  
1 5

<210> 56  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 56  
aaatgaaggga gaattattggt gttaactaggg

30

<210> 57  
<211> 30  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization probe

<400> 57

aaatgacata-gatcttttttt gttcctaggg

30

<210> 58

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization probe

<400> 58

aaatctcggga gaactcttggt gttcctaggg

30

<210> 59

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization probe

<400> 59

aaatgacgggt cactcttggt gttcctaggg

30

<210> 60

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization probe

<400> 60

aaatgacgctt ctcttttggt gttcctaggg

30

<210> 61

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization probe

<400> 61  
aaatcteggt cactcttggt gttcctaggg 30

<210> 62  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Description of Artificial Sequence: Hybridization  
probe

<400> 62  
aaatcagga gaacattggt gttcctaggg 30

<210> 63  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Description of Artificial Sequence: Hybridization  
probe

<400> 63  
aaatagagta gtactttggt gttcctaggg 30

<210> 64  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Description of Artificial Sequence: Hybridization  
probe

<400> 64  
aaatctegga gaacattggt gttcctaggg 30

<210> 65  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Description of Artificial Sequence: Hybridization  
probe

<400> 65  
aaatgacgt caacattggt gttcctaggg 30

<210> 66  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Hybridization  
 probe

<400> 66  
 aagggcggt caacttgggt gtctctaggg 30

<210> 67  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Hybridization  
 probe

<400> 67  
 aaatctgggt caacattggt gtctctaggg 30

<210> 68  
 <211> 158  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(153)

<400> 68  
 gag ggg aaa tat att cac cct caa aat aat tcg att tgc tgt acc aag 48  
 Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys  
 1 5 10 15

tgc cac aaa gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag 96  
 Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln  
 20 25 30

gat acg gac tgc agg gag tgt gag agc ggc tcc ttc aca gcc tca gaa 144  
 Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu  
 35 40 45

aac aac aag gatcc 158  
 Asn Asn Lys  
 50

<210> 69  
 <211> 51  
 <212> PRT  
 <213> Homo sapiens

<400> 69

Thr Gly Lys Tyr Ile His Pro His Asn Asn Ser Ile Cys Cys Thr Lys  
1 5 10 15

Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln  
20 25 30

Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu  
35 40 45

Asn Asn Lys  
50

<210> 70

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of Artificial Sequence: PCR primer  
EBI-1786

<400> 70

ggaattcagc ctgaatggcg aatggg 26

<210> 71

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of Artificial Sequence: PCR primer  
EBI-1729

<400> 71

ctctgagcgt tcttgccgtt ttccc 25

<210> 72

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of Artificial Sequence: PCR primer  
EBI-1733

<400> 72

gtctgacatt gattattgac tag 23

<210> 73

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer:  
EBI-1734

<400> 73

ggattctct atgaatctag cgt

15

<210> 74

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutagenesis  
primer EBI-1751

<400> 74

gtaattgaac tegtctctg

19

<210> 75

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutagenesis  
primer EBI-1857

<400> 75

gacaggggca gcagccgg

18

<210> 76

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide EBI-1823

<400> 76

aactctctgca ggtcgacatc gatggatcgg tacctcgagc ggccgcgaat tct

53

<210> 77

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide EBI-1829



<400> 77

ctagagaatt cggggcgct cgaggtacg gatccatga tctgacg caga 54

<210> 78

<211> 65

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide EBI-1820

<400> 78

agctctagag attcggggc gctcgaggta cggatccat cgaatcgac ctgcagaagc 60

ttg

63

<210> 79

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide EBI-1821

<400> 79

ctagcaagct tctcgaggtc gacatcgatg gatccggta ctcgagggc cgggaattct 60

ctag

64

<210> 80

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

EBI-1936

<400> 80

cagatccga gctcaaac ccaac

25

<210> 81

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

EBI-1929

<400> 81  
aggatttct tat taattct caatctgggg taggcacaa ttc 43

<210> 81  
<211> 81  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Description of Artificial Sequence: PCR primer  
EBI-2452

<400> 82  
aacatcgac ttacatttgc ttctgacac actgtgttca ctagsacct caaacagaca 60  
ccatgggect ctccaccgtg c 81

<210> 83  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Description of Artificial Sequence: PCR primer  
EBI-1922

<400> 83  
gaggetgcaa ttgaagc 17

<210> 84  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Description of Artificial Sequence: PCR primer  
EBI-2316

<400> 84  
attcttgagg cgccctag 17

<210> 85  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Description of Artificial Sequence: PCR primer  
EBI-2467

<400> 85  
gtcggtagca ccaagga 17

<210> 86  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-1986

<400> 86  
gttttccag taacgac 17

<210> 87  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Sequencing  
primer EBI-2112

<400> 87  
gtccaattat gtcacacc 18